

0590
1/09

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/978,522

DATE: 11/01/2001

TIME: 14:20:32

Input Set : A:\37890.txt

Output Set: N:\CRF3\11012001\I978522.raw

PS AE

5 <110> APPLICANT: Descenzo, Richard
7 Irelan, Nancy
11 <120> TITLE OF INVENTION: Lipoxxygenase Genes From Vitis Vinifera
15 <130> FILE REFERENCE: 29520/37890
C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/978,522
C--> 19 <141> CURRENT FILING DATE: 2001-10-16
19 <150> PRIOR APPLICATION NUMBER: 60/241,220
21 <151> PRIOR FILING DATE: 2000-10-16
25 <160> NUMBER OF SEQ ID NOS: 45
29 <170> SOFTWARE: PatentIn version 3.0
33 <210> SEQ ID NO: 1
35 <211> LENGTH: 862
37 <212> TYPE: PRT
39 <213> ORGANISM: Vitis LOX 1
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46 1 5 10 15
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51 Leu Asp Phe Asn Asp Phe Asn Ala Pro Val Arg Asp Arg Val His Glu
52 35 40 45
54 Leu Phe Gly Gln Gly Val Ser Leu Gln Leu Val Ser Ala Val His Gly
55 50 55 60
57 Asp Pro Ala Asn Gly Leu Gln Gly Lys Leu Gly Lys Pro Ala Tyr Leu
58 65 70 75 80
60 Glu Asp Trp Ile Thr Thr Ile Thr Ser Leu Thr Ala Gly Glu Ser Ala
61 85 90 95
63 Phe Lys Val Thr Phe Asp Trp Asp Glu Glu Ile Gly Glu Pro Gly Ala
64 100 105 110
66 Phe Ile Ile Arg Asn Asn His His Ser Glu Phe Tyr Leu Arg Thr Leu
67 115 120 125
69 Thr Leu Glu Asp Val Pro Gly Arg Gly Arg Ile His Phe Val Cys Asn
70 130 135 140
72 Ser Trp Val Tyr Pro Ala Lys His Tyr Lys Thr Asp Arg Val Phe Phe
73 145 150 155 160
75 Thr Asn Gln Thr Tyr Leu Pro Ser Glu Thr Pro Gly Pro Leu Arg Lys
76 165 170 175
78 Tyr Arg Lys Gly Glu Leu Val Asn Leu Arg Gly Asp Gly Thr Gly Glu
79 180 185 190
81 Leu Lys Glu Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu
82 195 200 205
84 Gly Lys Pro Asp Arg Asp Leu Lys Tyr Ala Arg Pro Val Leu Gly Gly
85 210 215 220
87 Ser Ala Glu Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Pro
88 225 230 235 240
90 Ser Glu Lys Asp Pro Lys Thr Glu Ser Arg Leu Pro Leu Val Met Ser
91 245 250 255

ENTERED

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93 Leu Asn Ile Tyr Val Pro Arg Asp Glu Arg Phe Gly His Leu Lys Met
94           260           265           270
96 Ser Asp Phe Leu Ala Tyr Ala Leu Lys Ser Ile Val Gln Phe Leu Leu
97           275           280           285
99 Pro Glu Phe Glu Ala Leu Cys Asp Ile Thr Pro Asn Glu Phe Asp Ser
100          290           295           300
102 Phe Gln Asp Val Leu Asp Leu Tyr Glu Gly Gly Ile Lys Val Pro Glu
103 305           310           315           320
105 Gly Pro Leu Leu Asp Lys Ile Lys Asp Asn Ile Pro Leu Glu Met Leu
106           325           330           335
108 Lys Glu Leu Val Arg Thr Asp Gly Glu His Leu Phe Lys Phe Pro Met
109           340           345           350
111 Pro Gln Val Ile Lys Glu Asp Lys Ser Ala Trp Arg Thr Asp Glu Glu
112           355           360           365
114 Phe Ala Arg Glu Met Leu Ala Gly Leu Asn Pro Val Val Ile Arg Leu
115           370           375           380
118 Leu Gln Glu Phe Pro Pro Lys Ser Lys Leu Asp Pro Glu Val Tyr Gly
119 385           390           395           400
121 Asn Gln Asn Ser Ser Ile Thr Lys Glu His Ile Glu Asn His Leu Asp
122           405           410           415
124 Asp Leu Thr Ile Asn Glu Ala Met Glu Lys Lys Arg Leu Phe Ile Leu
125           420           425           430
127 Asp His His Asp Val Phe Met Pro Tyr Leu Arg Arg Ile Asn Thr Thr
128           435           440           445
130 Ser Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Lys Asp Asp
131           450           455           460
133 Gly Thr Leu Lys Pro Leu Ala Ile Glu Leu Ser Leu Pro His Pro Asn
134 465           470           475           480
136 Gly Asp Lys Phe Gly Ala Val Asn Lys Val Tyr Thr Pro Ala Glu Asp
137           485           490           495
139 Gly Val Glu Gly Ser Ile Trp Gln Leu Ala Lys Ala Tyr Ala Ala Val
140           500           505           510
142 Asn Asp Ser Gly Tyr His Gln Leu Leu Ser His Trp Leu Asn Thr His
143           515           520           525
145 Ala Ala Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser Val
146           530           535           540
148 Leu His Pro Ile His Lys Leu Leu His Pro His Phe Arg Asp Thr Met
149 545           550           555           560
151 Asn Ile Asn Ala Leu Ala Arg Gln Ile Leu Ile Asn Ala Gly Gly Val
152           565           570           575
154 Val Glu Ser Thr Val Phe Pro Ser Lys Tyr Ala Met Glu Met Ser Ser
155           580           585           590
157 Val Val Tyr Lys Asp Trp Val Leu Thr Glu Gln Ala Leu Pro Ala Asp
158           595           600           605
160 Leu Ile Lys Arg Gly Met Ala Val Glu Asp Ser Glu Ala Pro His Gly
161           610           615           620
163 Leu Arg Leu Leu Ile Asp Asp Tyr Pro Tyr Ala Val Asp Gly Leu Glu
164 625           630           635           640
166 Ile Trp Ser Ala Ile Glu Thr Trp Val Lys Glu Tyr Cys Ser Phe Tyr

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167          645          650          655
169 Tyr Lys Thr Asp Glu Met Val Gln Lys Asp Ser Glu Leu Gln Ser Trp
170          660          665          670
172 Trp Lys Glu Val Arg Glu Glu Gly His Gly Asp Lys Lys Asp Glu Pro
173          675          680          685
176 Trp Trp Pro Lys Met Arg Thr Val Lys Glu Leu Ile Glu Thr Cys Thr
177          690          695          700
179 Ile Ile Ile Trp Val Ala Ser Ala Leu His Ala Ala Val Asn Phe Gly
180 705          710          715          720
182 Gln Tyr Pro Tyr Ala Gly Tyr Leu Pro Asn Arg Pro Thr Ile Ser Arg
183          725          730          735
185 Arg Phe Met Pro Glu Glu Gly Thr Pro Glu Tyr Glu Glu Leu Lys Ser
186          740          745          750
188 Asn Pro Asp Lys Ala Phe Leu Lys Thr Ile Thr Ala Gln Leu Gln Thr
189          755          760          765
191 Leu Leu Gly Ile Ser Leu Ile Glu Val Leu Ser Arg His Ser Ser Asp
192          770          775          780
194 Glu Val Tyr Leu Gly Gln Arg Asp Thr Pro Glu Trp Thr Leu Asp Thr
195 785          790          795          800
197 Thr Pro Leu Lys Ala Phe Glu Lys Phe Gly Arg Lys Leu Ala Asp Ile
198          805          810          815
200 Glu Glu Met Ile Ile Asp Arg Asn Gly Asn Glu Arg Phe Lys Asn Arg
201          820          825          830
203 Val Gly Pro Val Lys Ile Pro Tyr Thr Leu Leu Tyr Pro Thr Ser Glu
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206 Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile
207          850          855          860
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211 <211> LENGTH: 4687
213 <212> TYPE: DNA
215 <213> ORGANISM: Vitis LOX 1
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224 ccggttcggg accgggttca tgagcttttt ggacagggag tctctctgca gctcgtcagt      180
226 gctgttcatg gtgacctcgg tgagtttttt tttttttttt tttccttcat gtttttgatg      240
228 atgggggttg tgaagttgga ggagaggagg ttgataccgt tttgtgaggg tgagatgggt      300
230 tctgaatttt gatgatagca attggaaaaa gatgtgattt ttggaagagg ccaagagggg      360
232 ttgttattct cagagatgag tcaaatagact ttcttgacat cttccattca actgggcact      420
234 tttctaaactg cttttgtttt ttgtgttttg tttttaatgc ttttgttttc tacttctttc      480
236 tcttgtttat atttcttttc atcaaccact atacatgccc acctaaactca atatgaaatt      540
238 cccatgcagc tgcccttttt ttttaagccac tagatccttg gtgatttttt agtccttagat      600
240 cttgggttag atttccccag atttcacaaa agttgaaact gaaattcata aaatttttga      660
242 ggatcactcc tgttgagagt aaagagaaaag aattgccata aaccaaggag atgaattgtt      720
244 gtgaaatatt tctcaaaact tcatcatcaa atacctgcca aaacagccac agtttctgaa      780
246 atttcatgca gcaaagccac tgctgcttgt agcaagtcca agctcaaaca taaaagcctt      840
248 ttcaaccagc tgatttttga gaataacatg taaaaatgca gtgaccatct gttagtgatg      900
250 atattgaaact tgtgtgcctt ttgtagcaaa tgggttacag gggaaaacttg ggaaaccagc      960
252 atacttgga gactggatta ccacaattac ttctttaacc gctggcgagt ctgcattcaa      1020

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256	tcaccacagt	gagttttacc	tcaggactct	cactcttgaa	gatgttcctg	gacgtggcag	1140
258	aattcacttt	gtttgtaatt	cctgggtcta	ccctgctaag	cactacaaaa	ctgaccgtgt	1200
260	ttttcttact	aatcaggtaa	gactaatttg	cttgatacta	ggagagtctg	ctgtggcatt	1260
262	gtggccatt	gagcttaggc	aaggagaatt	gtctgctaaa	ggaatgtgtt	tattttatct	1320
264	gctgcagaca	tatcttccaa	gtgaaacacc	agggccactg	cgcaagtaca	gaaaagggga	1380
266	actggtgaat	ctgaggggag	atggaaccgg	agagcttaag	gaatgggatc	gagtgtatga	1440
268	ctatgcttac	tataatgatt	tggggaagcc	agacagggat	ctcaaataatg	cccgcctctg	1500
270	gctgggagga	tctgcagagt	atccttatcc	caggagggga	agaactggta	gaccaccatc	1560
272	tgaaaaaggt	agatatttga	tacacaaatt	catattgttt	ctcatgcttt	tatcataaaa	1620
274	ggatgaatat	gattgatttc	tgctcttctt	ttaattaaaca	gatcccaaaa	ctgagagcag	1680
276	attgccactt	gtgatgagct	taaacatata	tgttccaaga	gatgaacgat	ttggtcacct	1740
278	gaagatgtca	gacttcctgg	cttatgccct	gaaatccata	gttcaattcc	ttctccctga	1800
280	gtttgaggct	ctatgtgaca	tcacccccaa	tgagtttgac	agcttccaag	atgtattaga	1860
282	cctctacgaa	ggaggaatca	aggctccaga	gggcccttta	ctggacaaaa	ttaaggacaa	1920
284	catccctctt	gagatgctca	aggaacttgt	tcgtaccgat	ggggaacatc	tcttcaagtt	1980
286	cccaatgccc	caagtcatca	aaggtaactg	atacatctaa	catcttgtaa	tctttgaagc	2040
288	cagatttata	tattttattt	tcataaaatt	gatgacgttt	ttatcatgct	ggagcagagg	2100
290	ataagtctgc	atggaggact	gacgaagaat	ttgctagaga	aatgctggct	ggactcaacc	2160
292	cagttgtcat	cctgtacttc	caagtaaact	acagcttctt	ttcaaataat	ttttaatgcc	2220
294	ctgtttgttt	tctgagaaaa	tggaacttgg	aaaggcttcc	agactttgtt	ttctttccct	2280
296	ccatctactg	ttctagctct	tttctgataa	ttattggctc	tttctacttt	gtttgaagga	2340
298	gtttcctcca	aaaagcaagc	tggatcctga	agtttatggc	aacccaaaaca	gttcaataac	2400
300	caaagaacac	atagagaatc	acctggatga	ccttactata	aacgaggtaa	cgtcttagg	2460
302	ttccgttctt	tcaaaactaa	tttttcaatg	tcgacatgtt	aattttttgc	attggaacac	2520
304	aagccatagt	aactgaaaaa	tgggtgctttt	tactaggcaa	tggagaagaa	gaggctattc	2580
306	atattagatc	accatgatgt	tttcatgcca	tacctgagga	ggataaacac	aacttccacg	2640
308	aaaacttacg	cctcaaggac	tctcctcttc	ctgaaagacg	acggaacttt	gaagccactg	2700
310	gogattgaat	tgagcctacc	acatcctaatt	ggggataaaat	tcggagctgt	caacaaagta	2760
312	tacacaccag	ctgaagatgg	cgttgaaagt	tccatttggc	agctggctaa	agcttatgct	2820
314	gctgtgaatg	actctggcta	tcacagcttc	ctcagccact	ggtacgtaat	ctcccaaagg	2880
316	aaagtgcgta	cagttggggc	gtaaatctga	agcgggttat	gaatatcttt	gatgttggtt	2940
318	gcaggttgaa	tacacatgct	gcaattgagc	catttgatgat	tgcaaccaac	aggcagctca	3000
320	gtgtgcttca	cccaattcac	aagcttttgc	atcctcactt	ccgtgatacg	atgaatataa	3060
322	atgcattagc	tcgacaaatc	ctcatcaatg	ctgggtggagt	ggtggagagc	acagtttttc	3120
324	catcaaagta	tgccatggaa	atgtcatctg	ttgtttacaa	agactgggtt	ctcactgagc	3180
326	aagcacttcc	tgctgatctc	atcaagaggt	atataaatac	tgtagtgat	tgttttcttt	3240
328	cctgctgtgc	aatgaatcta	gtgaaaattg	tgattttcat	ctaactgata	tgctccaact	3300
330	tgggcactct	ttcagaggaa	tggcggttga	ggattcagag	gcccctcatg	gactccgcct	3360
332	actgatagat	gactacccct	atgctgttga	tggacttgag	atctgggtcag	ctattgagac	3420
334	atgggtgaaa	gagtattgct	cattctacta	caagacagat	gagatgggtcc	agaaagactc	3480
336	tgagcttcag	tcttgggtga	aggaagtcat	ggaagagggt	catggcgaca	agaaggacga	3540
338	gccttgggtg	cctaaaatgc	gtactgtcaa	agagctgata	gaaacatgca	ccattatcat	3600
340	ctgggtggct	tctgctctcc	atgctgcagt	gaatttcggg	cagtaccctt	atgcaggcta	3660
342	cctcccaaac	cgcccaacga	taagccgcag	attcatgcct	gaagaaggca	ctcctgagta	3720
344	tgaagaactc	aagtccaatc	ctgataaggc	tttcttgaaa	acaatcactg	cccagctgca	3780
346	gacccttctt	ggcatctccc	ttattgaggt	cctttccagg	cattcttccg	atgaggttta	3840
348	tcttggacag	agagacatct	ctgaatggac	cctggacaca	acaccattga	aagcttttga	3900
350	gaaattcggga	aggaagctgg	cagacattga	agaaatgatc	atagatagaa	atggaaaatga	3960

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352 gagattcaag aacagagttg ggcctgtgaa gataccatac acactgctct accccacaag 4020
354 cgaaggtggg cttactggca aagggattcc caacagtgtc tccatctaaa ttttcctgga 4080
356 aaatcatgag cacactgctg atcaagatgg cttaaagtca cattgctaata atagtatact 4140
358 gtaatttata atacctatitt ttcgactitt taggattcat attgatgcat atatttataa 4200
360 taaggaatta tttattgcta gaaaattggg agcttttcac tttttttatg atctgtgcca 4260
362 cacttaatgt taaaagatga aggtgaagta gcaaaacagt tgatctgaat gcgcagccat 4320
364 tgatatcagg aatcaaagtc agatggtgca aatgctctca aaacatccac cctcccacaa 4380
366 aattatctat aattttacatg ttaacaagaa ctcaagagtg agtaagaaac tatgttgaga 4440
368 aatactttct gaaaccactg aggaaagtgt ccatttgaag aagtgtgaga ctcttaccta 4500
370 agaagtgtct gtagatttga atagtaactg ccaatatctc tatcaaactc ttattattac 4560
372 atgtattaga ttttgatatg atgcttggat agtatgccta taaacaaatg catccccgag 4620
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376 gttgttg 4687
379 <210> SEQ ID NO: 3
381 <211> LENGTH: 859
383 <212> TYPE: PRT
385 <213> ORGANISM: Vitis LOX 2
389 <400> SEQUENCE: 3
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394 Lys Ile Lys Gly Thr Val Val Leu Met Lys Lys Asn Val Leu Asp Phe
395 20 25 30
397 Asn Asp Phe Asn Ala Ser Val Leu Asp Arg Val His Glu Leu Leu Gly
398 35 40 45
400 Gln Gly Val Pro Leu Gln Leu Val Ser Ala Val His Gly Asp Pro Ala
401 50 55 60
403 Asn Gly Leu Gln Gly Lys Ile Gly Lys Pro Ala Tyr Leu Glu Asp Trp
404 65 70 75 80
406 Ile Thr Thr Ile Thr Ser Leu Thr Ala Gly Glu Ser Ala Phe Lys Val
407 85 90 95
409 Thr Phe Asp Trp Asp Glu Glu Ile Gly Glu Pro Gly Ala Phe Ile Ile
410 100 105 110
412 Arg Asn Asn His His Ser Glu Phe Tyr Leu Arg Thr Leu Thr Leu Glu
413 115 120 125
415 Asp Val Pro Gly Arg Gly Arg Ile His Phe Val Cys Asn Ser Trp Val
416 130 135 140
418 Tyr Pro Ala Gln His Tyr Lys Thr Asp Arg Val Phe Phe Thr Asn Gln
419 145 150 155 160
421 Thr Tyr Leu Pro Ser Glu Thr Pro Gly Pro Leu Arg Lys Tyr Arg Glu
422 165 170 175
424 Gly Glu Leu Val Asn Leu Arg Gly Asp Gly Thr Gly Glu Leu Lys Glu
425 180 185 190
427 Trp Asp Arg Val Tyr Asp Tyr Ala Tyr Tyr Asn Asp Leu Gly Asn Pro
428 195 200 205
430 Asp Arg Asp Leu Lys Tyr Ala Arg Pro Val Leu Gly Gly Ser Ala Glu
431 210 215 220
433 Tyr Pro Tyr Pro Arg Arg Gly Arg Thr Gly Arg Pro Pro Ser Glu Lys
434 225 230 235 240
436 Asp Pro Asn Thr Glu Ser Arg Leu Pro Leu Val Met Ser Leu Asn Ile

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:19 M:270 C: Current Application Number differs, Replaced Current Application No
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:820 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:914 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1008 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10